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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/776,213	02/12/2004	Graham P. Belfield	3764-152	2071
23117	7590	03/10/2005	EXAMINER	
NIXON & VANDERHYE, PC 1100 N GLEBE ROAD 8TH FLOOR ARLINGTON, VA 22201-4714			LEFFERS JR, GERALD G	
		ART UNIT	PAPER NUMBER	1636

DATE MAILED: 03/10/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)
	10/776,213	BELFIELD ET AL.
	Examiner	Art Unit
	Gerald G. Leffers Jr., PhD	1636

— The MAILING DATE of this communication appears on the cover sheet with the correspondence address —
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
 - If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
 - If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
 - Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) Responsive to communication(s) filed on 17 December 2004.
 2a) This action is FINAL. 2b) This action is non-final.
 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) Claim(s) 1-29 is/are pending in the application.
 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
 5) Claim(s) _____ is/are allowed.
 6) Claim(s) 1-9, 11-18, 20 and 22-29 is/are rejected.
 7) Claim(s) 10, 19 and 21 is/are objected to.
 8) Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) The specification is objected to by the Examiner.
 10) The drawing(s) filed on 12 February 2004 is/are: a) accepted or b) objected to by the Examiner.
 Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
 Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
 a) All b) Some * c) None of:
 1. Certified copies of the priority documents have been received.
 2. Certified copies of the priority documents have been received in Application No. 09/743,194
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|--|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date <u>2/12/2004</u> . | 6) <input checked="" type="checkbox"/> Other: <u>Exhibit A; SEARCH RECD IT SEQ NO: 2</u> |



DETAILED ACTION

Election/Restrictions

Applicant's election of Group II (claims 1-29 directed to SEQ ID NO: 2) in the reply filed on 12/17//2004 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Information Disclosure Statement

Receipt is acknowledged of an information disclosure statement (IDS) filed on 2/12/2004. The signed and initialed PTO Form 1449 has been mailed with this action. The four search results (e.g. "B-Door External...") have not been considered as they were not present in the patent file. It is further noted that in any case there is no indication of the publication date for these references or where the information is available to the public (i.e. the publisher). If applicants want the information therein to be considered, the information should be resubmitted in a form consistent with 37 CFR 1.98.

Specification

The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

The following title is suggested: Compositions and Methods Using the Yeast HOR7 Promoter.

The disclosure is objected to because of the following informalities: at several places in the specification there are odd placements of letters and symbols at the beginning and ending of words. For example, on page 2 at lines 5 & 6, the term “Ayeast promoter@” is used. It appears as though the characters “A” and “@” are meant to be quotation marks around the word “yeast”. Another example occurs at page 25, line 14. Numerous instances of these typographical errors are present throughout the specification. It would be remedial to amend the specification in each instance to clearly indicate that what is intended.

Claim Objections

Claims 10 & 21 are objected to because of the following informalities: each recites nonelected inventions (i.e. the different vector constructs comprising the nonelected promoter elements). It would be remedial to amend the claims to be directed to the two elected embodiments (i.e. pYMR251AP + luc and pYMR251AP). Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-6 are rejected under 35 U.S.C. 101 because the claims read on nonstatutory subject matter. The claims are directed to “A yeast promoter which comprises at least [17, 50, 100, 200, 300 or 400] contiguous nucleotides of an isolated and purified polynucleotide which is SEQ ID NO: 2...” without any explicit limitation as to what context the promoter is found. The terms “isolated and purified polynucleotide” refer to SEQ ID NO:2 and not to the promoter that

is claimed. As written, the claim can be interpreted to encompass any promoter that meets the limitation of comprising at least 17 contiguous nucleotides of SEQ ID NO: 2, regardless of the context in which the promoter is found. By this interpretation, the rejected claims read on the native YMR251WA promoter.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-6 are rejected under 35 U.S.C. 102(b) as being anticipated by Hunt et al (see the attached search report for Accession No. Z48639) as evidenced by Goffeau et al (Science, 1996, Vol. 274, pages 546-567; see the entire reference).

Accession No. 48639 corresponds to *S. cerevisiae* cosmid clone 9920, which has 99.6 identity with SEQ ID NO: 2 over its entire length. The sequence of clone 9920 was submitted by Hunt et al as early as 10 March 1995 and was apparently available to the public as of 11 August 1997. Goffeau et al teach that the entire *S. cerevisiae* genomic sequence was known by October 1996.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-6, 8-9, 11-18, 20, 22-28 rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to a yeast promoter, vectors and host cells comprising the promoter. Some of the rejected claims are directed to methods of expressing a protein featuring the promoter, where the promoter comprises at least 17 contiguous nucleotides of SEQ ID NO: 2 and wherein the promoter can drive expression of a nucleic acid molecule encoding the polypeptide when operatively linked thereto. The promoter can be operative in any cell type (e.g. claims 1-6) or must at least be operative in yeast (e.g. claim 8). The promoter may have at least 50, 100, 200, 300, 400 contiguous nucleotides of SEQ ID NO: 2. Alternatively, the promoter can comprise the entire 723 nucleotides of SEQ ID NO:2. For many of the claims, the level of promoter activity is controlled by the level of fermentable carbon source (e.g. glucose) and/or non-fermentable carbon source (e.g. ethanol) in the culture medium.

SEQ ID NO: 2 describes a 723 nucleotide sequence. Even for embodiments featuring a promoter comprising as much as 400 contiguous nucleotides of SEQ ID NO: 2, there are a very large number of possible fragments of SEQ ID NO: 2 that may or may not retain promoter activity. As the number of contiguous nucleotides of SEQ ID NO: 2 that must be present in the claimed promoter or promoter fragment decreases, the number of possible fragments that must

function as a promoter greatly increases (e.g. 17 contiguous nucleotides out of 723). Thus, the claims are broad genus claims encompassing a large number of fragments of SEQ ID NO: 2 that must retain functional activity as a promoter element. The size of the genus is further compounded by the functional limitation in at least some of the claims that the promoter must be responsive to fermentable and non-fermentable carbon sources in culture media.

SEQ ID NO: 2 is 723 nucleotides in length and describes a sequence that is found at the beginning of the 7MR251WA (HOR7) reading frame (e.g. see Figure 14 of the instant specification). The specification describes the cloning of SEQ ID NO: 2 into an expression vector with an operatively linked reporter polypeptide (i.e. encoding luciferase) to demonstrate that the sequence described by SEQ ID NO: 2 has promoter activity and that the activity is responsive to both glucose and ethanol in culture media (e.g. Table 7). No description is provided, however, for any fragment of SEQ ID NO: 2 of any length that retains promoter activity. No description is provided in the instant specification for any sequence within SEQ ID NO: 2 that resembles any known transcription factor binding sequence (e.g. GAL4, etc.). The specification provides no guidance with regard to which fragments within SEQ ID NO: 2 might be essential for response to fermentable or non-fermentable carbon sources in culture media.

The prior art does not offset the deficiencies of the instant specification with regard to description of the claimed invention. Promoter sequences comprising SEQ ID NO: 2 do not appear to have been described in the prior art. While one of skill in the art might be able to identify sequences within SEQ ID NO: 2 that possess some homology to binding sites for known transcription factors, there may well be other unknown transcription factors required for even the basal level of promoter activity associated with SEQ ID NO: 2, much less glucose- or ethanol-

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responsive activities. Again, there is no description in the art of record for regulatory sequences that control expression of HOR7 in yeast.

Given the great number of possible fragments of SEQ ID NO: 2 encompassed by the rejected claims and the limitation that the fragments must retain at least some functional activity, and given the lack of a structural/functional basis in the instant specification or prior art for the skilled artisan to envision those embodiments that actually do retain promoter activity, the skilled artisan would not have been able to envision a sufficient number of the claimed embodiments to describe the broadly claimed genus. Therefore, the skilled artisan would have reasonably concluded applicants were not in possession of the claimed invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter that the applicant regards as his invention.

Claim 7 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 7 is vague and indefinite in that the metes and bounds of the phrase "which is SEQ ID NO: 2" are unclear. As written, the phrase can be applied to the "yeast promoter" itself, or alternatively, to the isolated and purified polynucleotide. It is thus unclear whether the claim is limited to SEQ ID NO: 2 or can encompass a promoter comprising sequences in addition to SEQ ID NO: 2.

Conclusion

Claims 1-9, 11-18, 20 & 22-28 are rejected. Claims 10, 19 & 21 are objected to as being directed to nonelected embodiments. Claim 29 is allowable.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gerald G. Leffers Jr., PhD whose telephone number is (571) 272-0772. The examiner can normally be reached on 6:30-4:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached on (571) 272-0781. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



GERRY LEFFERS
PRIMARY EXAMINER

Gerald G Leffers Jr., PhD
Primary Examiner
Art Unit 1636

ggl

Db	136	GGGGCTAAGACTTCTTCACCTTCTCCCTCATATCCTCCCTTATCCTPATCCCCCTGAGAACCCCTCT 195	Db	138	ACCTAAAGGAAAGGCTACCTTGAGGAAGGAGAACGGCTGTAAAGGGAT 197
Qy	181	CTCCCGCACGATTCTCCCTCATATCCTCCCTTATCCTPATCCCCCTGAGAACCC 240	Qy	121	GGGGCTAAGACTTCTTCACCTTCTCCCTTATCCTPATCCCCCTGAGAACCCCTCT 180
Db	196	CTCCCGCACGATTCTCCCTCATATCCTCCCTTATCCTPATCCCCCTGAGAACCC 255	Db	198	GGGGCTAAGACTTCTTCACCTTCTCCCTTATCCTPATCCCCCTGAGAACCCCTCT 257
Qy	241	GCACTATGACTAAATGGTGGAGACATCTCATGACTGACTGACTGTGATCTCACGT 300	Qy	181	CTCGCCGACGATTCTCCCTCATATCCTCCCTTATCCTPATCCCCCTGAGAACCC 240
Db	256	GCACTATGACTAAATGGTGGAGACATCTCATGACTGACTGACTGTGATCTCACGT 315	Db	258	CTCCCGCACGATTCTCCCTCATATCCTCCCTTATCCTPATCCCCCTGAGAACCC 317
Qy	301	GTTAAGGCCCGTGGCTCGGAACCGTTCTCTGACATTCTGACATTCTGACATTCTGACAGGGCTACA 360	Qy	241	GCACTATGACTAAATGGTGGAGACATCTCATGACTGACTGTGATCTCACAGT 300
Db	316	GTTAAGGCCCGTGGCTCGGAACGGTTCTCTGACATTCTGACATTCTGACAGGGCTACA 375	Db	318	GCACTATGACTAAATGGTGGAGACATCTCATGACTGACTGTGATCTCACAGT 377
Qy	361	GTCTCGATAATAGATAATAAAGCATTTTGCTGACGCCGGGCCGCTTTCCTA 420	Qy	301	GTTAACGGCACCGTGGCTGGAAACGGTTCTCTGACAACTTCTGACAGGGCTACA 360
Db	376	GTCTCGATAATAGATAATAAAGCATTTTGCTGACGCCGGGCCGCTTTCCTA 435	Db	378	GTTAACGGCACCGTGGCTGGAAACGGTTCTCTGACAACTTCTGACAGGGCTACA 437
Qy	421	ATAGGGAGGGCAGTTTATCGGGAGCTACTCTCTCTTATGGTAAGGCCCTTC 480	Qy	361	GTCMCGATAATAGATAATAAGGCATTTTGCTAGCCCGCGGGCCCTTTCCTA 420
Db	436	ATAGGGAGGGCAGTTTATCGGGAGCTACTCTCTCTTATGGTAAGGCCCTTC 495	Db	438	GTCMCGATAATAGATAATAAGGCATTTTGCTAGCCGGCGGGCTTTCCTA 497
Qy	481	TGTTTTCGGCAGTTTATGGCTGAGCTGAGCTTCTTATGGTAAGGGTGTAC 540	Qy	421	ATAGGGAGGGCAGTTTATGGCTGAGCTGAGCTTCTTATGGTAAGGGTGTAC 480
Db	496	TGTTTTCGGCAGTTTATGGCTGAGCTGAGCTTCTTATGGTAAGGGTGTAC 555	Db	498	ATAGGGAGGGCAGTTTATGGCTGAGCTTCTTATGGTAAGGGTGTAC 557
Qy	541	TTCGATGAAAGGAATTAGCAAGGGAAAAAAACTATGGCTAGCTGGATTTCTCA 600	Qy	481	TGTTTTCGGCAGTTTATGGCTGAGCTGAGCTGAGCTTCTTATGGTAAGGGTGTAC 540
Db	556	TTCGATGAAAGGAATTAGCAAGGGAAAAAAACTATGGCTAGCTGGATTTCTCA 615	Db	558	TGTTTTCGGCAGTTTATGGCTGAGCTGAGCTGAGCTTCTTATGGTAAGGGTGTAC 617
Qy	601	TCATATAAAAGGGAATTGGCTCAGCTATGGCTAGCTTCTGGACTCTTAACCTT 660	Qy	541	TTCGATGAAAGGAATTAGCAAGGGAAAAAAACTATGGCTAGCTGGAGTTCTCA 600
Db	616	TCATATAAAAGGGAATTGGCTCAGCTATGGCTAGCTTCTGGACTCTTAACCTT 675	Db	618	TTCGATGAAAGGAATTAGCAAGGGAAAAAAACTATGGCTAGCTGGAGTTCTCA 677
Qy	661	TATTGAGGAGGACTCAATCATACAGATTGTCAAAGGCTTAATAATA 720	Qy	601	TCATATAAAAGGGAATTGGCTCAGCTATGGCTAGCTGGAGTTCTGGAGCTTCTCA 660
Db	676	TATTGAGGAGGACTCAATCATACAGATTGTCAAAGGCTTAATAATA 735	Db	678	TCATATAAAAGGGAATTGGCTCAGCTATGGCTAGCTGGAGTTCTGGAGCTTCTCA 737
Qy	721	CAT 723	Qy	661	TATTGAGGAGGACTCAATCATACAGATTGTCAAAGGCTTAATAATA 720
Db	736	CAT 738	Db	738	TATTGAGGAGGACTCAATCATACAGATTGTCAAAGGCTTAATAATA 797
Qy	721	CA 722	Qy	721	CA 722
Db	798	AA 799	Db	798	AA 799
RESULT 4					
LOCUS	AR492055	AR492055	850 bp	DNA	linear
DEFINITION	Sequence 30 from patent US 6716801.			PAT 15-MAY-2004	
ACCESSION	AR492055				RESULT 5
VERSION	AR492055.1	GI : 47260524			SC9920
KEYWORDS				SC9920	23498 bp
SOURCE	Unknown.			LOCUS	DNA
ORGANISM	Unclassified.			DEFINITION	chromosome XIII cosmid 9920.
REFERENCE	1 (bases 1 to 850)			VERSION	Z48639.1 GI:732924
AUTHORS	Belfield, G.P. and Oakley, C.			KEYWORDS	COX7; cytochrome oxidase; delta element; glutamate decarboxylase; PET111; transfer RNA- <i>Ala</i> .
TITLE	Compositions and methods utilizing the yeast ZE01 promoter			SOURCE	Saccharomyces cerevisiae (baker's yeast)
JOURNAL	Patent : US 671601-A 30 06-APR-2004;			ORGANISM	Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomyces.
FEATURES	Location:Qualifiers			REFERENCE	Saccharomyctales; Saccharomyces; Saccharomyces.
source	1..850			AUTHORS	Hunt, S. and Bowman, S.
	/organism="unknown"			COMMENT	Unpublished (bases 1 to 23498) Barrell, B., Rayandream, M.A. and Walsh, S.V. Direct Submission Title Journal
ORIGIN	/mol_type="genomic DNA"			REFERENCE	Barrell, B., Rayandream, M.A. and Walsh, S.V. Best Local Similarity 99.9%; Pred. No. 2.4e-206; Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query Match	99.6%	Score 720.4; DB 6; Length 850;		AUTHORS	Submitted (10-MAR-1995) Saccharomyces cerevisiae chromosome XIII sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: barrell@sanger.ac.uk
Best Local Similarity	99.9%	Pred. No. 2.4e-206;		COMMENT	Notes: All CDS over 100 codons have been analysed. CDS that are completely overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this analysis.
Matches	721	Matches 1;			
Qy	1	CTTCGATTAGCACATGAGCTGAGCTCATAGACTGGCTATAACACTAGGGAAA 60			
Db	78	CTTCGATTAGCACATGAGCTGAGCTCATAGACTGGCTATAACACTAGGGAAA 137			
Qy	61	ACCATAAAGGAAAGGCTAACCTACTTGGAGGAAAGGAGCACGCCCTTAAGGGAT 120			

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Exh.6.1A

Applicant Copy

Details of the omitted CDS are available on request. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons and the calculated codon adaptation index (CAI) is given for each CDS.

Cosmid 9920 is overlapped at the start of this sequence by cosmid 9408 and at the end of this sequence by cosmid 8156.

Location/Qualifiers

1..23498
organism="Saccharomyces cerevisiae"
mol_type="genomic DNA"
strain="AB972"
chromosome="XII"
clone="cosmid 9920"
complement(1.. 2870)
note="YMR920_01c, unknown, partial, len: 956, CAI: 0.14; PS00061 Short-chain alcohol dehydrogenase family signature"
codon_start=1

/protein_id="CAA88574_1"
db_xref="UniProt/Swiss-Prot:Q04781"
map="GI:732925"
*translation="MSSEGINTEQONTDGLIGHGIVRISLNVDGLDPSSLINSLYS NEKUCIFPSLKLQRDEETKALMDSIQNTEFLCWSKSPNLNEITCPS YKVRQLSHQITMLVSKRKISKPLDFPILLGCFELDSVSKSPNLNEITCPS KDPAKTNAWFOBQNLIVCEIVVNNEMEDEDEKRSKKESEFRHRVPAVLL LIKLEFHVKDOSRNSSLKVLISLTHIRLKVCPVPSLNLATLDDYEDGTWYDKS MPSHRKNMKLAVERKULSLTHIRLKVCPVPSLNLATLDDYEDGTWYDKS SKEKVKLKFSLVSRTPSPGPFNAVALYESTKHSFELDKYLEMPPHQKSVQLNLKG PSARNSASLVEFWTFNLKFAEDINSLBSYTKLNQTLISLDEKPLDQVQVLL GVPFDKWRBEIDFTSDERDIRKIKVSPEKRNFKVSEILVNTSPNNEAISRLDFDVQLL YSNSEKSPKQNTKYDGYDDALAYFLDSMIDMIFNGKIGKFEINRIPTVQYESQYONPAGIMAQ LYIEDEMKNTKFDDGEIKGNKPNFLQNQTITLYRASANGYOVEOFCAVLSLDETF FSTLJLNTDPLSCALYEVSDTNKELFLKLSLQAGKNSBIAQVILQHAGYVFSP GAKEKVKVTHAVELINGCNNTDQIOPPANALEPARVNHHVAFITVYDLSLSTITHLLP TDDPFLNKINQKLRYTAFLDALLDALPERVNHHVAFITVYDLSLSTITHLLP DLYYDGFHTKPKGRKVNQDLSVNGVNIOPANGEDAMLTIDIEASNSVTFYTSRVLY KVLLNLSIDTVTSSTTGLNLASLAESEVTXTRDQSSTDYLL".
complement(2406.. 2418)
note="PS00061 Short-chain alcohol dehydrogenase family signature"
complement(3200.. 3272)
note="tRNA-Ala"
product="tRNA-Ala, anticodon agc, len: 73"
complement(3379.. 3706)
note="delta element"
complement(join(4101.. 4196, 4691.. 4780))
note="YMR920_02c, unknown, len: 61, CAI: 0.17, possible small spliced gene"
*codon_start=1**

/product="unknown"
protein_id="CAA88575_1"
db_xref="GI:732926"
translation="TMEELAPMNKEDEGITNMCCQSLYRQYQIMRNSIGLRRLPLANKAIPNSL IPNLNSLALAHLCALYTE"
complement(join(4101.. 4196.. 4434.. 4505))
note="YMR920_03c, unknown, len: 55, CAI: 0.13, possible small spliced gene"
codon_start=1

/product="unknown"
protein_id="CAA88576_1"
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translation="TMEELAPMNKEDEGITNMCCQSLYRQYQIMRNSIGLRRLPLANKAIPNSL IPNLNSLALAHLCALYTE"
complement(41197.. 4199)
note="possible splice acceptor sequence, cag"

source

misc_feature
note="possible splice branch sequence, tactaac"
complement(4422.. 4428)
note="possible donor sequence, gatgtg"
complement(4428.. 4431)
note="possible donor sequence, gtcagt"
complement(4685.. 4690)
note="possible donor sequence, gtcagt"
complement(4689.. 4694)
note="possible donor sequence, gtcagt"
5632.. 7389
note="YMR920_04, unknown, len: 585, CAI: 0.18, putative glutamate decarboxylase gene"
codon_start=1
product="unknown"
protein_id="CAA88577_1"
db_xref="GI:732228"
db_xref="SGD:S004792"
db_xref="UniProt/Swiss-Prot:Q04792"
translation="MHRHGSQKONPNENIAGKVKVHDLAGLQLISNDVQKSAVOSGHQG SNMRDTSQGHANKTSVSPKQELPADISQMLQHWNPDIEPIGATPVSHRSHM RKLIDENLNTADNDYPOBLTERTCISQMLQHWNPDIEPIGATPVSHRSHM CGHAMKCRWEHMKNACKDASKPNLIMSSACOVALEKPTRYVEECRVLVPHDWSNTDIPIA DEASGGTIPPFGEKEKMAKYMERNMCFNPHRVSUTSGHKPGLTGPGLGHLWRE SULLADEURFKLKYLGGYEETGUNFSRPGFOVHOENEVSUGHSGYRTQFONSFLYVA RAPESELISSKLPGCPEVSSSASPSSASPSVQYRFGVPLVPLDQ YKKEFPEVPOPAILSLLRGRGWILPNYLPKATDSDKEVLRVYVFRSENMLDQI LLIIVDIESILTLKLHSTEYKCHIELASEOTPERKSSFUYIEMULALASPODDIPTPDE 7746.. 8846
note="YMR920_05, unknown, len: 366, CAI: 0.11, similar to YK56_YEAST_P36156, YKR076W, hypothetical protein in SIS2, 6. 6% identity in 369 aa overlap"
codon_start=1
product="unknown"
protein_id="CAA88578_1"
db_xref="GI:732229"
db_xref="SGD:S004863"
db_xref="UniProt/Swiss-Prot:Q04806"
translation="MSERKSASNNKQAFKRSQPFRELLSDHPIKPAGKRYWYALAL PCPWAQTLITRAUKGHALPILGCSVAHWHLDDKGMPFLIEGDKTNERHWFDIAGGIS SUNLNFTSPVANIPIHNARHLLVDCDTEPHGYKLSDFYKTKDYGKTFVPLNDL ETCIVANESSDQJIGIMNSAAFPDEFQDLYEQLTENSWYQDVKING VYKAGFACAEVYREVTSFQYDLCLENLDDKCYTDLAEYQGNKKDKLDRYPAIG DPLTEADYRVLPTIVEFEDVYHOHFKCNLATIIRDYDSRHTWLKNIYWRHERPQTID PTHIKLGYSRSPRNFQGIRPLGPKDPRIP"

CDS

note="YMR920_06c, unknown, len: 134, CAI: 0.13"

codon_start=1

product="unknown"

protein_id="CAA88579_1"

db_xref="GI:732300";

db_xref="SGD:S004865"

db_xref="UniProt/Swiss-Prot:Q04814"

translation="MIGKVFVSYIRPLSTNVSLSKGUSGMDEINDSPREVEGFYNDWK HBLANMSQBFQRFQGVNYRIOQSPSSNTNVSLSKGUSGMDEINDSPREVEGFYNDWK

complement(10146.. 10550)

note="YMR920_07c, unknown, len: 414, CAI: 0.13, hydrophobic domains"

codon_start=1

product="unknown"

protein_id="CAA88580_1"

db_xref="GI:732931"

db_xref="SGD:Q04835"

db_xref="UniProt/Swiss-Prot:Q04835"

translation="WNPSPVCKMRENTNTHVSKENMDTSLOLPSTTRSLSPKESNS NEDENVTGNETTQLQRISKDVKPNIGVILTVSYFENSAMVYSTKVLENDPDIANDR QIKPLQIQLVNRVITYGTLIYVSPFGRKPERXWLVRGCTGFGVPM YSYSLMLTISDVALITPLAPSITIIFSWVILRERFTRKVEALGSLISLGGVUVLVRBFL LGTPELTDSQSSQVSSDPSRLIARIUVGWLUGMSCYTIIYVIGRAHAIMSUS YFSLITAVISFIGINTPSMKFQIPIHSKQWILFGNLGVSSPFIQJLTMGIQRERAG

FEATURES

source

misc_feature

note="possible splice branch sequence, tactaac"

complement(4422.. 4428)

note="possible donor sequence, gatgtg"

complement(4428.. 4431)

note="possible donor sequence, gtcagt"

complement(4685.. 4690)

note="possible donor sequence, gtcagt"

complement(4689.. 4694)

note="possible donor sequence, gtcagt"

complement(4719.. 4726)

note="possible splice acceptor sequence, cag"

complement(4727.. 4734)

note="possible splice acceptor sequence, cag"

complement(4735.. 4742)

note="possible splice acceptor sequence, cag"

complement(4743.. 4750)

note="possible splice acceptor sequence, cag"

complement(4751.. 4758)

note="possible splice acceptor sequence, cag"

complement(4759.. 4766)

note="possible splice acceptor sequence, cag"

complement(4767.. 4774)

note="possible splice acceptor sequence, cag"

complement(4775.. 4782)

note="possible splice acceptor sequence, cag"

complement(4783.. 4790)

note="possible splice acceptor sequence, cag"

complement(4791.. 4798)

note="possible splice acceptor sequence, cag"

complement(4799.. 4806)

note="possible splice acceptor sequence, cag"

complement(4807.. 4814)

note="possible splice acceptor sequence, cag"

complement(4815.. 4822)

note="possible splice acceptor sequence, cag"

complement(4823.. 4830)

note="possible splice acceptor sequence, cag"

complement(4831.. 4838)

note="possible splice acceptor sequence, cag"

complement(4839.. 4846)

note="possible splice acceptor sequence, cag"

complement(4847.. 4854)

note="possible splice acceptor sequence, cag"

complement(4855.. 4862)

note="possible splice acceptor sequence, cag"

complement(4863.. 4870)

note="possible splice acceptor sequence, cag"

complement(4871.. 4878)

note="possible splice acceptor sequence, cag"

complement(4879.. 4886)

note="possible splice acceptor sequence, cag"

complement(4887.. 4894)

note="possible splice acceptor sequence, cag"

complement(4895.. 4902)

note="possible splice acceptor sequence, cag"

complement(4903.. 4910)

note="possible splice acceptor sequence, cag"

complement(4911.. 4918)

note="possible splice acceptor sequence, cag"

complement(4919.. 4926)

note="possible splice acceptor sequence, cag"

complement(4927.. 4934)

misc_feature

note="possible splice branch sequence, tactaac"

complement(4422.. 4428)

note="possible donor sequence, gatgtg"

complement(4428.. 4431)

note="possible donor sequence, gtcagt"

complement(4685.. 4690)

note="possible donor sequence, gtcagt"

complement(4689.. 4694)

note="possible donor sequence, gtcagt"

complement(4719.. 4726)

note="possible splice gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_03c, unknown, len: 55, CAI: 0.13, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_02c, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_01c, unknown, len: 55, CAI: 0.13, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_00c, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_00b, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_00a, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_009, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_008, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_007, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_006, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_005, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_004, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_003, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_002, unknown, len: 61, CAI: 0.17, possible small spliced gene"

complement(join(4101.. 4196.. 4434.. 4505))

note="YMR920_001, unknown, len: 61, CAI: 0.17, possible small spliced gene"

